

SEQUENCE LISTING

- (2) INFORMATION FOR SEQ ID NO: 68:
- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 34 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:
- GACTCGCTGC AGATCGATTT TTTTTTTTTT TTTT 34
- (2) INFORMATION FOR SEQ ID NO: 69:
- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 30 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:
- GCCATCAAGC CACCCAAGAA CTCTTA ACTT 30
- (2) INFORMATION FOR SEQ ID NO: 70:
- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 30 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:
- CCAATAGCCA GACCATTATA TACTACTAATT 30
- (2) INFORMATION FOR SEQ ID NO: 112:
- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 310 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GCTTATAGAA GGACCCCTAG TATGGGGTAA TCCCCTCTGG GAAACCAAGC CCCAGTACTC 60
AGCAGGAAAA ATAGAATAGG AAACCTCACA AGGACATACT TTCCTCCCCCT CCAGATGGCT 120
AGCCACTGAG GAAGGAAAAA TACTTTCACC TGCAGCTAAC CAACAGAAAT TACTTAAAC 180
CCTTCACCAA ACCTTCCACT TAGGCATTGA TAGCACCAAT CAGATGGCCA AATTATTATT 240
TACTGGACCA GGCCTTTTCA AAACATCAAA GAAGATAGTC AGGGGCTGTG AAGTGTGCCA 300
AAGAAATAAT 310

(2) INFORMATION FOR SEQ ID NO: 113:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Leu Ile Glu Gly Pro Leu Val Trp Gly Asn Pro Leu Trp Glu Thr Lys
1 5 10 15
Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His
20 25 30
Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu
35 40 45
Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr
50 55 60
Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe
65 70 75 80
Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys
85 90 95
Glu Val Cys Gln Arg Asn Asn
100

(2) INFORMATION FOR SEQ ID NO: 114:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

CCCTGTATCT TTAACCTCCT TGTTAAGTTT GTCTCTTCCA GAATCAAAAC TGTAAACTA 60
CAAATTGTTT TCAAATGGA GCACCAGATG GAGTCCATGA CTAAGATCCA CCGTGGACCC 120
CTGGACCGGC CTGCTAGCCC ATGCTCCGAT GTTAATGACA TTGAAGGCAC CCCTCCGAG 180
GAAATCTCAA CTGCACAACC CCTACTATGC CCCAATTCAG CGGGAAGCAG TTAGACCGGT 240
CATCAGCCAA CCTCCCCAAC AGCACTTGGG TTTTCCTGTT GAGAGGGGGG ACTGAGAGAC 300
AGGACTAGCT GGATTTCTTA GGCCAACGAA GAATCCCTAA GCCTAGCTGG GAAGGTGACT 360
GCATCCACCT CTAAACATGG GGCTTGCAAC TTAGCTCACA CCGGACCAAT CAGAGAGCTC 420
ACTAAAATGC TAATTAGGCA AAAATAGGAG GTAAAGAAAT AGCCAATCAT CTATTGCCTG 480
AGAGCACAGC GGGAGGGACA AGGATCGGGA TATAAACCCA GGCATTGAG CCGGCAACGG 540
CAACCCCTT TGGGTCCCCT CCCTTTGTAT GGGCGCTCTG TTTTACTCT ATTTCCTCT 600
ATTAAATCTT GCAACTGAAA AAAAAAAAAA AAAAA 635

(2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile Lys
1 5 10 15
Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser
20 25 30
Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys
35 40 45
Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr
50 55 60
Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TGGGGTTCCA TTTGTAAGAC CATCTGTAGC TT

32

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1481 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATGGCCCTCC CTTATCATAC TTTTCTCTTT ACTGTTCTCT TACCCCTTT CGCTCTCACT 60
GCACCCCTC CATGCTGCTG TACAACCACT AGCTCCCTT ACCAAGAGTT TCTATGAAGA 120
ACGCGGCTTC CTGGAATAT TGATGCCCCA TCATATAGGA GTTTATCTAA GGGAACTCC 180
ACCTTCACTG CCCACACCCA TATGCCCCGC AACTGCTATA ACTGTGCCAC TCTTTGCATG 240
CATGCAATA CTCATTATTG GACAGGGAAA ATGATTATC CTAGTTGTCC TGGAGGACTT 300
GGAGCCACTG TCTGTTGGAC TTACTTCACC CATACCAGTA TGTCTGATGG GGGTGGATT 360
CAAGGTCAGG CAAGAGAAAA ACAAGTAAAG GAAGCAATCT CCCAACTGAC CCGGGGACAT 420
AGCACCCCTA GCCCCTACAA AGGACTAGTT CTCTCAAAC TACATGAAAC CCTCCGTACC 480
CATACTCGCC TGGTGAGCCT ATTTAATACC ACCCTCACTC GGCTCCATGA GGTCTCAGCC 540
CAAAACCTA CTAAGTGTG GATGTGCTC GGCCTGCACT TCAGGCCATA CATTTCATC 600
CCTGTTCTG AACAAATGAA CAATTTCAGC ACAGAAATA ACACCACTTC CGTTTTAGTA 660
GGACCTCTTG TTTCCAATCT GGAATAACC CATACTCAA ACCTCACCTG TGTAATAATT 720
AGCAATACTA TAGACACAAC CAGCTCCTAA TGCATCAGGT GGGTAACACC TCCCACAGCA 780
ATAGTCTGCC TACCCTCAGG AATATTTTT GTCTGTGTA CCTCAGCCTA TCATTGTTG 840
AATGGCTCTT CAGAATCTAT GTGCTTCTC TCATTCTTAG TGCCCCCTAT GACCATCTAC 900
ACTGAACAAG ATTTATACAA TCATCTGTA CCTAAGCCCC ACAACAAAAG AGTACCCATT 960
CTTCCTTTTG TTATCAGAGC AGGAGTGCTA GGCAGACTAG GTACTGGCAT TGGCAGTATC 1020

ACAACCTCTA CTCAGTTCTA CTACAACTA TCTCAAGAAA TAAATGGTGA CATGGAACAG 1080
 GTCAGTACT CCCTGGTCAC CTTGCAAGAT CAACTTAACCT CCCTAGCAGC AGTAGTCCTT 1140
 CAAAATCGAA GAGCTTTAGA CTTGCTAACC GCCAAAAGAG GGGGAACCTG TTTATTTTAA 1200
 GGAGAAGAAC GCTGTTATTA TGTTAATCAA TCCAGAATTG TCACTGAGAA AGTTAAAGAA 1260
 ATTCGAGATC GAATACAATG TAGAGCAGAG GAGCTTCAAA ACACCGAACG CTGGGGCCTC 1320
 CTCAGCCAAT GGATGCCCTG GGTTCTCCCC TTCTTAGGAC CTCTAGCAGC TCTAATATTG 1380
 TTAATCCTCT TTGGACCCTG TATCTTTAAC CTCCTTGTTA AGTTTGTCTC TTCCAGAATT 1440
 GAAGCTGTAA AGCTACAGAT GGTCTTACAA ATGGAACCCC A 1481

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 493 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Met Ala Leu Pro Tyr His Thr Phe Leu Phe Thr Val Leu Leu Pro Pro
 1 5 10 15
 Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser
 20 25 30
 Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp
 35 40 45
 Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala
 50 55 60
 His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met
 65 70 75 80
 His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
 85 90 95
 Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr
 100 105 110
 Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln
 115 120 125
 Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser
 130 135 140
 Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr

145	150	155	160
His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His			
165	170	175	
Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu			
180	185	190	
His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn			
195	200	205	
Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val			
210	215	220	
Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe			
225	230	235	240
Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr			
245	250	255	
Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys			
260	265	270	
Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys			
275	280	285	
Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp			
290	295	300	
Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile			
305	310	315	320
Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly			
325	330	335	
Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln			
340	345	350	
Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu			
355	360	365	
Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg			
370	375	380	
Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu			
385	390	395	400
Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu			
405	410	415	
Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu			
420	425	430	
Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val			

435 440 445
 Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Leu Phe
 450 455 460
 Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile
 465 470 475 480
 Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro
 485 490

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TCAAAATCGA AGAGCTTTAG ACTTGCTAAC CG 32

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1329 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

TCAAAATCGA AGAGCTTTAG ACTTGCTAAC CGCCAAAAGA GGGGGAACCT GTTTATTTTT 60
 AGGGGAAGAA TGCTGTTAGT ATGTTAATCA ATCTGGAATC ATTACTGAGA AAGTTAAAGA 120
 AATTGAGAT CGAATATAAT GTAGAGCAGA GGACCTTCAA AACACTGCAC CCTGGGGCCT 180
 CCTCAGCCAA TGGATGCCCT GGACTCTCCC CTTCTTAGGA CCTCTAGCAG CTATAATATT 240
 TTTACTCCTC TTTGGACCCT GTATCTTCAA CTTCTTCTT AAGTTTGTCT CTTCCAGAAT 300
 TGAAGCTGTA AAGCTACAAA TAGTTCTTCA AATGGAACCC CAGATGCAGT CCATGACTAA 360
 AATCTACCGT GGACCCCTGG ACCGGCCTGC TAGACTATGC TCTGATGTTA ATGACATTGA 420
 AGTCACCCCT CCCGAGGAAA TCTCAACTGC ACAACCCCTA CTACACTCCA ATTCACTAGG 480
 AAGCAGTTAG AGCAGTTGTC AGCCAACCTC CCCAACAGTA CTTGGGTTTT CTTGTTGAGA 540
 GGGTGGACTG AGAGACAGGA CTAGCTGGAT TTCCTAGGCT GACTAAGAAT CCCNAAGCCT 600

ANCTGGGAAG GTGACCGCAT CCATCTTTAA ACATGGGGCT TGCAACTTAG CTCACACCCG 660
 ACCAATCAGA GAGCTCACTA AAATGCTAAT CAGGCAAAAA CAGGAGGTAA AGCAATAGCC 720
 AATCATCTAT TGCCTGAGAG CACAGCGGGA AGGACAAGGA TTGGGATATA AACTCAGGCA 780
 TTCAAGCCAG CAACAGCAAC CCCCTTTGGG TCCCCTCCCA TTGTATGGGA GCTCTGTTTT 840
 CACTCTATTT CACTCTATTA AATCATGCAA CTGCACTCTT CTGGTCCGTG TTTTTATGG 900
 CTCAAGCTGA GCTTTTGTTC GCCATCCACC ACTGCTGTTT GCCACCGTCA CAGACCCGCT 960
 GCTGACTTCC ATCCCTTTGG ATCCAGCAGA GTGTCCACTG TGCTCCTGAT CCAGCGAGGT 1020
 ACCCATTGCC ACTCCCGATC AGGCTAAAGG CTTGCCATTG TTCCTGCATG GCTAAGTGCC 1080
 TGGGTTTGTG CTAATAGAAC TGAACACTGG TCACTGGCTT CCATGGTTCT CTTCATGAC 1140
 CCACGGCTTC TAATAGAGCT ATAACACTCA CCGCATGGCC CAAGATTCCA TTCCTTGTA 1200
 TCTGTGAGGC CAAGAACCC AGGTCAGAGA ANGTCAGGCT TGCCACCATT TGGGAAGTGG 1260
 CCCACTGCCA TTTTGGTAGC GGCCCAACCAC CATCTGGGA GCTGTGGGAG CAAGGATCCC 1320
 CCAGTAACA 1329

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Gln	Asn	Arg	Arg	Ala	Leu	Asp	Leu	Leu	Thr	Ala	Lys	Arg	Gly	Gly	Thr
1				5					10					15	
Cys	Leu	Phe	Leu	Gly	Glu	Glu	Cys	Cys	Xaa	Tyr	Val	Asn	Gln	Ser	Gly
			20						25					30	
Ile	Ile	Thr	Glu	Lys	Val	Lys	Glu	Ile	Xaa	Asp	Arg	Ile	Xaa	Cys	Arg
			35						40					45	
Ala	Glu	Asp	Leu	Gln	Asn	Thr	Ala	Pro	Trp	Gly	Leu	Leu	Ser	Gln	Trp
			50						55					60	
Met	Pro	Trp	Thr	Leu	Pro	Phe	Leu	Gly	Pro	Leu	Ala	Ala	Ile	Ile	Phe
			65						70					75	
Leu	Leu	Leu	Phe	Gly	Pro	Cys	Ile	Phe	Asn	Phe	Leu	Val	Lys	Phe	Val
			85						90					95	
Ser	Ser	Arg	Ile	Glu	Ala	Val	Lys	Leu	Gln	Ile	Val	Leu	Gln	Met	Glu
			100						105					110	

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg
 115 120 125
 Pro Ala Arg Leu Cys Ser Asp Val Asn Asp Ile Glu Val Thr Pro Pro
 130 135 140
 Glu Glu Ile Ser Thr Ala Gln Pro Leu Leu His Ser Asn Ser Val Gly
 145 150 155 160
 Ser Ser

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

10 GGCATTGATA GCACCCATCA G 21

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

20 CATGTCACCA GGCTGGAATA G 21

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 758 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GGCATTGATA GCACCCATCA GATGGCCAAA TCATTATTTA CTGGACCAGG CCTTTTCAAA 60
ACTATCAAGC AGATAGGGCC CGTGAAGCAT GCCAAAGAAA TAATCCCCTG CTTATCGCC 120
ATGTTCTTTC AGGAGAACAA AGAACAGGCC ATTACCCAGG GGAAGACTGG CAACTAGATT 180
TTACCCACAT GGCCAAATGT CAGGGATTTC AGCATCTACT AGTCTGGGCA GATACTTTCA 240
CTGGTTGGGT GGAGTCTTCT CTTGTAGGA CAGAAAAGAC CCAAGAGGTA ATAAAGGCAC 300
TAATGAAATA ATTCCCAGAT TTGGACTTCC CCCAGGATTA CAGGGTGACA ATGGCCCCGC 360
TTTCAAGGCT GCAGTAACCC AGGGAGTATC CCAGGTGTTA GCCATACAAT ATCACTTACA 420
CTGTGCCTGG AGGCCACAAT CCTCCAGAAA AGTCAAGAAA ATGAATGAAA CACTCAAAGA 480
TCTAAAAAAG CTAACCCAAG AAACCCACAT TGCATGACCT GTTCTGTTGC CTATAACCTT 540
ACTAAGAATC CATAACTATC CCCCAGAAA CAGGACTTAG CCCATACGAG ATGCTATATG 600
GATGGCCTTT CCTAACCAAT GACCTTGTC TTGACTGAGA AATGGCCAAC TTAGTTGCAG 660
ACATCACCTC CTTAGCCAAA TATCAACAAG TTCTTAAAC ATCACAGGGA ACCTGTCCCC 720
GAGAGGAGGG AAAGGAAC TAACCCCTG GTGACATG 758

10 (2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

CGGACATCCA AAGTGATGGG AAACG

25

20 (2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

REPLACEMENT SHEET (RULE 26)

GGACAGGAAA GTAAGACTGA GAAGGC

26

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCTAGAACGT ATTCTGGAGA ATTGGG

26

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 26 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGGCTCTCAA TGGTCAAACA TACCCG

26

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1511 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CCTAGAACGT ATTCTGGAGA ATTGGGACCA ATGTGACACT CAGACGCTAA GAAAGAAACG 60

ATTTATATTC TTCTGCAGTA CCGCCTGGCC ACAATATCCT CTTCAAGGGA GAGAAACCTG 120
 GCTTCCTCAG GGAAGTATAA ATTATAACAT CATCTTACAG CTAGACCTCT TCTGTAGAAA 180
 GGAGGGCAAA TGGAGTGAAG TGCCATATGT GCAAACCTTC TTTTCATTAA GAGACAACTC 240
 ACAATTATGT AAAAAGTGTG GTTTATGCCC TACAGGAAGC CCTCAGAGTC CACCTCCCTA 300
 CCCCAGCGTC CCCTCCCCGA CTCCTTCCTC AACTAATAAG GACCCCCCTT TAACCCAAAC 360
 GGTCCAAAAG GAGATAGACA AAGGGGTAAA CAATGAACCA AAGAGTGCCA ATATTCCCCG 420
 ATTATGCCCC CTCCAAGCAG TGAGAGGAGG AGAATTCCGC CCAGCCAGAG TGCCTGTACC 480
 TTTTCTCTCT TCAGACTTAA AGCAAATTAA AATAGACCTA GGTAAATTCT CAGATAACCC 540
 TGACGGCTAT ATTGATGTTT TACAAGGGTT AGGACAATCC TTTGATCTGA CATGGAGAGA 600
 TATAATGTTA CTAATAATC AGACACTAAC CCCAATGAG AGAAGTGCCG CTGTAACCTG 660
 AGCCCCGAGAG TTTGGCGATC TTTGGTATCT CAGTCAGGCC AACAAATAGGA TGACAACAGA 720
 GGAAAGAACA ACTCCACAG GCCAGCAGGC AGTTCCTCAGT GTAGACCCTC ATTGGGACAC 780
 AGAATCAGAA CATGGAGATT GGTGCCACAA ACATTGCTA ACTTGGCTG TAGAAGGACT 840
 GAGGAAAAC AGGAAGAAGC CTATGAATTA CTCAATGATG TCCACTATAA CACAGGGAAA 900
 GGAAGAAAAT CTTACTGCTT TTCTGGACAG ACTAAGGGAG GCATTGAGGA AGCATACCTC 960
 CCTGTCACTT GACTCTATTG AAGGCCAACT AATCTTAAAG GATAAGTTTA TCACTCAGTC 1020
 AGCTGCAGAC ATTAGAAAAA ACTTCAAAG TCTGCCTTAG GCGCGGAGCA GAACTTAGAA 1080
 ACCCTATTTA ACTTGGCATC CTCAGTTTTT TATAATAGAG ATCAGGAGGA GCAGGCCGAA 1140
 CGGGACAAAC GGGATAAAAA AAAAAGGGGG GGTCCACTAC TTTAGTCATG GCGCTCAGGC 1200
 AAGCAGACTT TGGAGGCTCT GCAAAGGGGA AAGCTGGGC AAATCAAATG CCTAATAGGG 1260
 CTGGCTTCCA GTGCGGTCTA CAAGGACACT TAAAAAAGA TTATCCAAGT AGAAATAAGC 1320
 CGCCCCCTTG TCCATGCCCC TTACGTCAAG GGAATCACTG GAAGGCCAC TGCCCCAGGG 1380
 GATGAAGATA CTCTGAGTCA GAAGCCATTA ACCAGATGAT CCAGCAGCAG GACTGAGGGT 1440
 GCGCGGGGCG AGCGCCAGCC CATGCCATCA CCTCACAGA GCGCGGGTA TGTTTGACCA 1500
 TTGAGAGCCA A 1511

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu

10

1

5

10

15

Arg	Lys	Lys	Arg	Phe	Ile	Phe	Phe	Cys	Ser	Thr	Ala	Trp	Pro	Gln	Tyr	
			20					25					30			
Pro	Leu	Gln	Gly	Arg	Glu	Thr	Trp	Leu	Pro	Glu	Gly	Ser	Ile	Asn	Tyr	
		35					40					45				
Asn	Ile	Ile	Leu	Gln	Leu	Asp	Leu	Phe	Cys	Arg	Lys	Glu	Gly	Lys	Trp	
		50				55					60					
Ser	Glu	Val	Pro	Tyr	Val	Gln	Thr	Phe	Phe	Ser	Leu	Arg	Asp	Asn	Ser	
65				70						75				80		
Gln	Leu	Cys	Lys	Lys	Cys	Gly	Leu	Cys	Pro	Thr	Gly	Ser	Pro	Gln	Ser	
			85					90						95		
Pro	Pro	Pro	Tyr	Pro	Ser	Val	Pro	Ser	Pro	Thr	Pro	Ser	Ser	Thr	Asn	
			100					105						110		
Lys	Asp	Pro	Pro	Leu	Thr	Gln	Thr	Val	Gln	Lys	Glu	Ile	Asp	Lys	Gly	
		115				120						125				
Val	Asn	Asn	Glu	Pro	Lys	Ser	Ala	Asn	Ile	Pro	Arg	Leu	Cys	Pro	Leu	
		130				135					140					
Gln	Ala	Val	Arg	Gly	Gly	Glu	Phe	Gly	Pro	Ala	Arg	Val	Pro	Val	Pro	
145				150					155					160		
Phe	Ser	Leu	Ser	Asp	Leu	Lys	Gln	Ile	Lys	Ile	Asp	Leu	Gly	Lys	Phe	
			165					170					175			
Ser	Asp	Asn	Pro	Asp	Gly	Tyr	Ile	Asp	Val	Leu	Gln	Gly	Leu	Gly	Gln	
		180						185					190			
Ser	Phe	Asp	Leu	Thr	Trp	Arg	Asp	Ile	Met	Leu	Leu	Leu	Asn	Gln	Thr	
		195				200							205			
Leu	Thr	Pro	Asn	Glu	Arg	Ser	Ala	Ala	Val	Thr	Ala	Ala	Arg	Glu	Phe	
		210				215							220			
Gly	Asp	Leu	Trp	Tyr	Leu	Ser	Gln	Ala	Asn	Asn	Arg	Met	Thr	Thr	Glu	
225					230					235				240		
Glu	Arg	Thr	Thr	Pro	Thr	Gly	Gln	Gln	Ala	Val	Pro	Ser	Val	Asp	Pro	
			245					250						255		
His	Trp	Asp	Thr	Glu	Ser	Glu	His	Gly	Asp	Trp	Cys	His	Lys	His	Leu	
		260						265					270			
Leu	Thr	Cys	Val	Leu	Glu	Gly	Leu	Arg	Lys	Thr	Arg	Lys	Lys	Pro	Met	
		275					280						285			
Asn	Tyr	Ser	Met	Met	Ser	Thr	Ile	Thr	Gln	Gly	Lys	Glu	Glu	Asn	Leu	
		290					295						300			

1	5	10	15
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg			
20	25	30	
Ile Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr			
35	40	45	
Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln			
50	55	60	
Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn			
65	70	75	80
Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys			
85	90	95	
Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn			
100	105	110	
Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln			
115	120	125	
Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr			
130	135	140	
Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys			
145	150	155	160
Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro			
165	170	175	
Leu Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val			
180	185	190	
Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys			
195	200	205	
Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly			
210	215	220	
Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln			
225	230	235	240
Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu			
245	250	255	
Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr			
260	265	270	
Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp			
275	280	285	
Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His			

290	295	300
Leu Leu Thr Cys Val	Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro	
305	310	315 320
Met Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn		
325	330	335
Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr		
340	345	350
Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys		
355	360	365
Phe Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu		
370	375	380
Pro Lys Leu Ala Ala Ala Leu Glu His His His His His His		
385	390	395

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Leu Glu Arg		
1	5	10 15
Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu Arg Lys Lys		
20	25	30
Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr Pro Leu Gln		
35	40	45
Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr Asn Ile Ile		
50	55	60
Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp Ser Glu Val		
65	70	75 80
Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser Gln Leu Cys		
85	90	95
Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser Pro Pro Pro		
100	105	110

Tyr	Pro	Ser	Val	Pro	Ser	Pro	Thr	Pro	Ser	Ser	Thr	Asn	Lys	Asp	Pro
115							120					125			
Pro	Leu	Thr	Gln	Thr	Val	Gln	Lys	Glu	Ile	Asp	Lys	Gly	Val	Asn	Asn
130						135					140				
Glu	Pro	Lys	Ser	Ala	Asn	Ile	Pro	Arg	Leu	Cys	Pro	Leu	Gln	Ala	Val
145					150					155				160	
Arg	Gly	Gly	Glu	Phe	Gly	Pro	Ala	Arg	Val	Pro	Val	Pro	Phe	Ser	Leu
			165					170					175		
Ser	Asp	Leu	Lys	Gln	Ile	Lys	Ile	Asp	Leu	Gly	Lys	Phe	Ser	Asp	Asn
		180						185					190		
Pro	Asp	Gly	Tyr	Ile	Asp	Val	Leu	Gln	Gly	Leu	Gly	Gln	Ser	Phe	Asp
	195						200					205			
Leu	Thr	Trp	Arg	Asp	Ile	Met	Leu	Leu	Leu	Asn	Gln	Thr	Leu	Thr	Pro
210						215					220				
Asn	Glu	Arg	Ser	Ala	Ala	Val	Thr	Ala	Ala	Arg	Glu	Phe	Gly	Asp	Leu
225					230					235				240	
Trp	Tyr	Leu	Ser	Gln	Ala	Asn	Asn	Arg	Met	Thr	Thr	Glu	Glu	Arg	Thr
			245						250				255		
Thr	Pro	Thr	Gly	Gln	Gln	Ala	Val	Pro	Ser	Val	Asp	Pro	His	Trp	Asp
		260						265					270		
Thr	Glu	Ser	Glu	His	Gly	Asp	Trp	Cys	His	Lys	His	Leu	Leu	Thr	Cys
		275					280					285			
Val	Leu	Glu	Gly	Leu	Arg	Lys	Thr	Arg	Lys	Lys	Pro	Met	Asn	Tyr	Ser
	290					295					300				
Met	Met	Ser	Thr	Ile	Thr	Gln	Gly	Lys	Glu	Glu	Asn	Leu	Thr	Ala	Phe
305					310						315			320	
Leu	Asp	Arg	Leu	Arg	Glu	Ala	Leu	Arg	Lys	His	Thr	Ser	Leu	Ser	Pro
		325							330				335		
Asp	Ser	Ile	Glu	Gly	Gln	Leu	Ile	Leu	Lys	Asp	Lys	Phe	Ile	Thr	Gln
	340					345						350			
Ser	Ala	Ala	Asp	Ile	Arg	Lys	Asn	Phe	Lys	Ser	Leu	Pro	Lys	Leu	Ala
	355					360						365			
Ala	Ala	Leu	Glu	His	His	His	His	His	His						
370						375									

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:
CTTGGAGGGT GCATAACCAG GGAAT 25

5

(2) INFORMATION FOR SEQ ID NO: 139:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleotide
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:
TGTCGCTGT GTCCTGATC 20

15

(2) INFORMATION FOR SEQ ID NO: 140:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleotide
20 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:
CTATGTCCTT TTGGACTGTT TGGGT 25

25

(2) INFORMATION FOR SEQ ID NO: 141:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 764 base pairs
(B) TYPE: nucleotide
30 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGTCGGCTGT	GCTCCTGATC	CAGCACAGGC	GCCCATTTGCC	TCTCCCAATT	GGGCTAAAGG	60
CTTGCCATTG	TTCCTGCACA	GCTAAGTGCC	TGGGTTTCATC	CTAATCGAGC	TGAACACTAG	120
TCACTGGGTT	CCACGGTTCT	CTTCCATGAC	CCATGGCTTC	TAATAGAGCT	ATAACACTCA	180
CTGCATGGTC	CAAGATTCCA	TTCCTTGGA	TCCGTGAGAC	CAAGAACCCC	AGGTCAGAGA	240
ACACAAGGCT	TGCCACCATG	TTGGAAGCAG	CCCACCACCA	TTTTGGAAGC	AGCCCGCCAC	300
TATCTTGGGA	GCTCTGGGAG	CAAGGACCCC	AGGTAACAAT	TTGGTGACCA	CGAAGGGACC	360
TGAATCCGCA	ACCATGAAGG	GATCTCCAAA	GCAATTGGAA	ATGTTCTCTC	CAAGGCCAAA	420
ATGCCCCTAA	GATGTATTCT	GGAGAATTGG	GACCAATTTG	ACCCTCAGAC	AGTAAGAAAA	480
AAATGACTTA	TATTCTTCTG	CAGTACCGCC	CTGGCCACGA	TATCCTCTTC	AAGGGGGAGA	540
AACCTGGCCT	CCTGAGGGAA	GTATAAATTA	TAACACCATC	TTACAGCTAG	ACCTGTTTTG	600
TAGAAAAGGA	GGCAAATGGA	GTGAAGTGCC	ATATTTACAA	ACTTTCTTTT	CATTAAAAGA	660
CAACTCGCAA	TTATGTTAAC	ACTGTGATTT	GTGTTCTTAC	ACGGAAGCCC	TCAGATTCTA	720
CTCCCCACCC	CCGGCATCTC	CCCTGAATCC	CTCCCCAACT	TATT		764

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

TGTCGGCTGT	GCTCCTGATC	CAGCACAGGC	GCCCATTTGCC	TCTCCCAATT	GGGCTAAAGG	60
CTTGCCATTG	TTCCTGCACA	GCTAAGTGCC	TGGGTTTCATC	CTAATCGAGC	TGAACACTAG	120
TCACTGGGTT	CCACGGTTCT	CTTCCATGAC	CCATGGCTTC	TAATAGAGCT	ATAACACTCA	180
CTGCATGGTC	CAAGATTCCA	TTCCTTGGA	TCCGTGAGAC	CAAGAACCCC	AGGTCAGAGA	240
ACACAAGGCT	TGCCACCATG	TTGGAAGCAG	CCCACCACCA	TTTTGGAAGC	AGCCCGCCAC	300
TATCTTGGGA	GCTCTGGGAG	CAAGGACCCC	CAGGTAACAA	TTTGGTGACC	ACGAAGGGAC	360
CTGAATCCGC	AACCATGAAG	GGATCTCCAA	AGCAATTGGA	AATGTTCTCT	CCAAGGCCAA	420
AATGCCCCTA	AGATGTATTC	TGGAGAATTG	GGACCAATCT	GACCCCTCAG	CAGTAAGAAA	480
AAAAATGACT	TATATTCTTC	TGCAGTACCG	CCTGGCCATG	GATATCCTCT	TCAAGGGGGA	540
GAAACCTGGC	CTCCTGAGGG	AAGTATAAAT	TATAACACCA	TCTTACAGCT	AGACCTGTTT	600
TGTAGAAAAG	GAGGCATAATG	GAGTGAAGTG	CCATATTTAC	AACTTTCTTT	TTCAATAAAA	660
GACAACTCGC	AATTATGTAA	ACAGTGTGAT	TTGTGTCCTA	CAGGAAGCCC	TCAGATCTAC	720
CTCCCTACCC	CGGCATCTCC	CTGACTCCTT	CCCCAACTAA	TAAGGACCCA	CTTCAGCCCA	780
AACAGTCCAA	AAGGACATAG					800